STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: *10/785,220A*
Source: *FRW976*
Date Processed by STIC: *4-6-05*

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE <u>CHECKER VERSION 4.2.2 PROGRAM</u>, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05): U.S. Patent and Trademark Office. Mail Stop Sequence. Customer Window. Randolph Building. 401 Dulany Street. Alexandria, VA 22314

Revised 01/24/05

ERROR DETECTED   **SUGGESTED CORRECTION**   SERIAL NUMBER: 10/785,220A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 _____ Wrapped Nucleics / Wrapped Aminos — The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .): this will prevent "wrapping."

2 _____ Invalid Line Length — The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 _____ Misaligned Amino Numbering — The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4 _____ Non-ASCII — The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5 _____ Variable Length — Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing

6 _____ PatentIn 2.0 "bug" — A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7 _____ Skipped Sequences (OLD RULES) — Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence
(2) INFORMATION FOR SEQ ID NO X (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION SEQ ID NO X (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(i) NUMBER OF SEQUENCES" response to include the skipped sequences.

8 _____ Skipped Sequences (NEW RULES) — Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence
<210> sequence id number
<400> sequence id number
000

9 _____ Use of n's or Xaa's (NEW RULES) — Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<221> is MANDATORY if n's or Xaa's are present
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents

10 _____ Invalid <213> Response — Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence or scientific name (Genus/species). <220>-<221> section is required when <213> response is Unknown or is Artificial Sequence

11 _____ Use of <220> — Use of <220> to <223> is MANDATORY if <213> Organism response is "Artificial Sequence" or "Unknown". Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol 63, No 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

12 _____ PatentIn 2.0 "bug" — Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 _____ Misuse of n/Xaa — "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid

AMC – Biotechnology Systems Branch – 09/09/2003

IFW16

```
      RAW SEQUENCE LISTING                    DATE: 04/06/2005
      PATENT APPLICATION:  US/10/785,220A     TIME: 14:13:57

      Input Set : A:\39780-1216.TXT
      Output Set: N:\CRF4\04062005\J785220A.raw

 4 <110> APPLICANT: Ashkenazi, Avi J.
 5         Fong, Sherman
 6         Goddard, Audrey
 7         Gurney, Austin L.
 8         Napier, Mary A.
 9         Tumas, Daniel
10         Wood, William I.
12 <120> TITLE OF INVENTION: COMPOUNDS, COMPOSITIONS AND METHODS FOR
13        THE TREATMENT OF DISEASES CHARACTERIZED BY A33- RELATED
14        ANTIGENS
16 <130> FILE REFERENCE: P1216R1C1D4
18 <140> CURRENT APPLICATION NUMBER: 10/785,220A
19 <141> CURRENT FILING DATE: 2004-02-24
21 <150> PRIOR APPLICATION NUMBER: US 09/254,465
22 <151> PRIOR FILING DATE: 1999-03-05
24 <150> PRIOR APPLICATION NUMBER: PCT/US98/24855
25 <151> PRIOR FILING DATE: 1998-11-20
27 <150> PRIOR APPLICATION NUMBER: US 60/066,364
28 <151> PRIOR FILING DATE: 1997-11-21
30 <150> PRIOR APPLICATION NUMBER: US 60/078,936
31 <151> PRIOR FILING DATE: 1998-03-20
33 <150> PRIOR APPLICATION NUMBER: PCT/US98/19437
34 <151> PRIOR FILING DATE: 1998-09-17
36 <160> NUMBER OF SEQ ID NOS: 30
38 <170> SOFTWARE: FastSEQ for Windows Version 4.0
40 <210> SEQ ID NO: 1
41 <211> LENGTH: 299
42 <212> TYPE: PRT
43 <213> ORGANISM: Homo sapiens
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49             20                  25                  30
50 Ser Ser Glu Pro Glu Val Arg Ile Pro Glu Asn Asn Pro Val Lys Leu
51         35                  40                  45
52 Ser Cys Ala Tyr Ser Gly Phe Ser Ser Pro Arg Val Glu Trp Lys Phe
53     50                  55                  60
54 Asp Gln Gly Asp Thr Thr Arg Leu Val Cys Tyr Asn Asn Lys Ile Thr
55 65                  70                  75                  80
56 Ala Ser Tyr Glu Asp Arg Val Thr Phe Leu Pro Thr Gly Ile Thr Phe
57                 85                  90                  95
58 Lys Ser Val Thr Arg Glu Asp Thr Gly Thr Tyr Thr Cys Met Val Ser
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RAW SEQUENCE LISTING   DATE: 04/06/2005
PATENT APPLICATION: US/10/785,220A   TIME: 14:13:57

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Output Set: N:\CRF4\04062005\J785220A.raw

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63      130                135                140
64 Ile Gly Asn Arg Ala Val Leu Thr Cys Ser Glu Gln Asp Gly Ser Pro
65 145                150                155                160
66 Pro Ser Glu Tyr Thr Trp Phe Lys Asp Gly Ile Val Met Pro Thr Asn
67                165                170                175
68 Pro Lys Ser Thr Arg Ala Phe Ser Asn Ser Ser Tyr Val Leu Asn Pro
69           180                185                190
70 Thr Thr Gly Glu Leu Val Phe Asp Pro Leu Ser Ala Ser Asp Thr Gly
71           195                200                205
72 Glu Tyr Ser Cys Glu Ala Arg Asn Gly Tyr Gly Thr Pro Met Thr Ser
73      210                215                220
74 Asn Ala Val Arg Met Glu Ala Val Glu Arg Asn Val Gly Val Ile Val
75 225                230                235                240
76 Ala Ala Val Leu Val Thr Leu Ile Leu Leu Gly Ile Leu Val Phe Gly
77           245                250                255
78 Ile Trp Phe Ala Tyr Ser Arg Gly His Phe Asp Arg Thr Lys Lys Gly
79           260                265                270
80 Thr Ser Ser Lys Lys Val Ile Tyr Ser Gln Pro Ser Ala Arg Ser Glu
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83      290                295
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87 <211> LENGTH: 321
88 <212> TYPE: PRT
89 <213> ORGANISM: Homo sapiens
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94 Thr Tyr Gly Arg Pro Ile Leu Glu Val Pro Glu Ser Val Thr Gly Pro
95           20                25                30
96 Trp Lys Gly Asp Val Asn Leu Pro Cys Thr Tyr Asp Pro Leu Gln Gly
97      35                40                45
98 Tyr Thr Gln Val Leu Val Lys Trp Leu Val Gln Arg Gly Ser Asp Pro
99      50                55                60
100 Val Thr Ile Phe Leu Arg Asp Ser Ser Gly Asp His Ile Gln Gln Ala
101 65                70                75                80
102 Lys Tyr Gln Gly Arg Leu His Val Ser His Lys Val Pro Gly Asp Val
103           85                90                95
104 Ser Leu Gln Leu Ser Thr Leu Glu Met Asp Asp Arg Ser His Tyr Thr
105           100                105                110
106 Cys Glu Val Thr Trp Gln Thr Pro Asp Gly Asn Gln Val Val Arg Asp
107      115                120                125
108 Lys Ile Thr Glu Leu Arg Val Gln Lys Leu Ser Val Ser Lys Pro Thr
109      130                135                140
110 Val Thr Thr Gly Ser Gly Tyr Gly Phe Thr Val Pro Gln Gly Met Arg
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RAW SEQUENCE LISTING   DATE: 04/06/2005
PATENT APPLICATION: US/10/785,220A   TIME: 14:13:57

Input Set : A:\39780-1216.TXT
Output Set: N:\CRF4\04062005\J785220A.raw

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112 Ile Ser Leu Gln Cys Gln Ala Arg Gly Ser Pro Pro Ile Ser Tyr Ile
113                 165                 170                 175
114 Trp Tyr Lys Gln Gln Thr Asn Asn Gln Glu Pro Ile Lys Val Ala Thr
115             180                 185                 190
116 Leu Ser Thr Leu Leu Phe Lys Pro Ala Val Ile Ala Asp Ser Gly Ser
117         195                 200                 205
118 Tyr Phe Cys Thr Ala Lys Gly Gln Val Gly Ser Glu Gln His Ser Asp
119     210                 215                 220
120 Ile Val Lys Phe Val Val Lys Asp Ser Ser Lys Leu Leu Lys Thr Lys
121 225                 230                 235                 240
122 Thr Glu Ala Pro Thr Thr Met Thr Tyr Pro Leu Lys Ala Thr Ser Thr
123             245                 250                 255
124 Val Lys Gln Ser Trp Asp Trp Thr Thr Asp Met Asp Gly Tyr Leu Gly
125             260                 265                 270
126 Glu Thr Ser Ala Gly Pro Gly Lys Ser Leu Pro Val Phe Ala Ile Ile
127         275                 280                 285
128 Leu Ile Ile Ser Leu Cys Cys Met Val Val Phe Thr Met Ala Tyr Ile
129     290                 295                 300
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137 <211> LENGTH: 390
138 <212> TYPE: DNA
139 <213> ORGANISM: Artificial Sequence
141 <220> FEATURE:
142 <223> OTHER INFORMATION: Artificial sequence
144 <400> SEQUENCE: 3
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146 ttgtatggtc tctgaggaag gcggcaacag ctatggggag gtcaaggtca agctcatcgt 120
147 gcttgtgcct ccatccaagc ctacagttaa catcccctcc tctgccacca ttgggaaccg 180
148 ggcagtgctg acatgctcag aacaagatgg ttccccacct tctgaataca cctggttcaa 240
149 agatgggata gtgatgccta cgaatcccaa aagcacccgt gccttcagca actcttccta 300
150 tgtcctgaat cccacaacag gagagctggt ctttgatccc ctgtcagcct ctgatactgg 360
151 agaatacagc tgtgaggcac ggaatgggta 390
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155 <212> TYPE: DNA
156 <213> ORGANISM: Artificial Sequence
158 <220> FEATURE:
159 <223> OTHER INFORMATION: Artificial sequence
161 <400> SEQUENCE: 4
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163 ctgttgtgct caggtgcgcc tgatcgcgat ggggacaaag gcgcaagctc gagaggaaac 120
164 tgttgtgcct cttcatattg gcgatcctgt tgtgctccct ggcattgggc agtgttacag 180
165 ttgcactctt ctgaacctga agtcagaatt cctgagaata atcctgtgaa gttgtcctgt 240
166 gcctactcgg gctttttcttc tccccgtgtg gagtggaagt ttgaccaagg agacaccacc 300
167 agactcgttt gctataataa caagatcaca gcttcctatg aggaccgggt gaccttcttg 360
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pls explain source of genetic material

Invalid Responce

pls explain source of genetic material

Invalid Response

pls see item# 11 on error summary sheet.

Input Set : A:\39780-1216.TXT
Output Set: N:\CRF4\04062005\J785220A.raw

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169 gtctctgagg aaggcggcaa cagctatggg gaggtcaagg tcaagctcat cgtgcttgtg 480
170 cctccatcca agcctacagt taacatcccc tcctctgcca ccattgggaa ccgggcagtg 540
171 ctgacatgct cagaacaaga tggttcccca ccttctgaat acacctggtt caaagatggg 600
172 atagtgatgc ctacgaatcc caaaagcacc cgtgccttca gcaactcttc ctatgtcctg 660
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178 <212> TYPE: DNA
179 <213> ORGANISM: Artificial Sequence
181 <220> FEATURE:
182 <223> OTHER INFORMATION: Artificial sequence
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187 gactcctgat ggcaaccaag tcgtgagaga taagattact gagctccgtg tccagaaact 180
188 ctctgtctcc aagcccacag tgacaactgg cagcggttat ggcttcacgg tgccccaggg 240
189 aatgaggatt agccttcaat gccagggttc ggggttctcc tcccatcagt tatatttggt 300
190 ataagcaaca gactaataac cagggaaccc atcaaagtag caaccctaag taccttactc 360
191 ttcaagcctg cggtgatagc cgactcaggc tcctatttct gcactgccaa gggccaggtt 420
192 ggctctgagc agcacagcga cattgtgaag tttgtggtca aagactcctc aaagctactc 480
193 aagaccaaga ctgaggcacc tacaaccatg acatacccct tgaaagcaac atctacagtg 540
194 aagcagtcct gggactggac cactgacatg gatggctacc ttggagagac cagtgctggg 600
195 ccaggaaaga gcctgcctgt ctttgccatc atcctcatca tctccttgtg ctgtatggtg 660
196 gtttttacca tggcctatat catgctctgt cggaagacat cccaacaaga gcatgtctac 720
197 gaagcagcca gggcacatgc cagagaggcc aacgactctg agaaaccat gagggtggcc 780
198 atcttcgcaa gtggctgctc cagtgatgag ccaacttccc agaatctggg gcaacaacta 840
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202 tgccttctgc atggccttct tccctgctac ctctcttcct ggatagccca aagtgtccgc 1080
203 ctaccaacac tggagccgct gggagtcact ggctttgccc tggaatttgc cagatgcatc 1140
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205 ctggtactcc tctctaaata ccagagggaa gatgcccata gcactaggac ttggtcatca 1260
206 tgcctacaga cactattcaa ctttggcatc ttgccaccag aagacccgag gggaggctca 1320
207 gctctgccag ctcagaggac cagctatatc caggatcatt tctctttctt cagggccaga 1380
208 cagcttttaa ttgaaattgt tatttcacag gccagggttc agttctgctc ctccactata 1440
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210 aaa                                                            1503
212 <210> SEQ ID NO: 6
213 <211> LENGTH: 319
214 <212> TYPE: PRT
215 <213> ORGANISM: Homo sapiens
217 <400> SEQUENCE: 6
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219 1               5                   10                  15
220 Val Thr Val Asp Ala Ile Ser Val Glu Thr Pro Gln Asp Val Leu Arg
221                 20                  25                  30
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[Handwritten annotations: "See error explanation. See item #11 on error summary sheet." "Invalid response" near line 182. "1503" correction near line 210. Circled note at bottom right: "The type of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors."]

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222 Ala Ser Gln Gly Lys Ser Val Thr Leu Pro Cys Thr Tyr His Thr Ser
223         35              40              45
224 Thr Ser Ser Arg Glu Gly Leu Ile Gln Trp Asp Lys Leu Leu Leu Thr
225     50              55              60
226 His Thr Glu Arg Val Val Ile Trp Pro Phe Ser Asn Lys Asn Tyr Ile
227 65              70              75              80
228 His Gly Glu Leu Tyr Lys Asn Arg Val Ser Ile Ser Asn Asn Ala Glu
229             85              90              95
230 Gln Ser Asp Ala Ser Ile Thr Ile Asp Gln Leu Thr Met Ala Asp Asn
231         100             105             110
232 Gly Thr Tyr Glu Cys Ser Val Ser Leu Met Ser Asp Leu Glu Gly Asn
233         115             120             125
234 Thr Lys Ser Arg Val Arg Leu Leu Val Leu Val Pro Pro Ser Lys Pro
235     130             135             140
236 Glu Cys Gly Ile Glu Gly Glu Thr Ile Ile Gly Asn Asn Ile Gln Leu
237 145             150             155             160
238 Thr Cys Gln Ser Lys Glu Gly Ser Pro Thr Pro Gln Tyr Ser Trp Lys
239             165             170             175
240 Arg Tyr Asn Ile Leu Asn Gln Glu Gln Pro Leu Ala Gln Pro Ala Ser
241         180             185             190
242 Gly Gln Pro Val Ser Leu Lys Asn Ile Ser Thr Asp Thr Ser Gly Tyr
243         195             200             205
244 Tyr Ile Cys Thr Ser Ser Asn Glu Glu Gly Thr Gln Phe Cys Asn Ile
245     210             215             220
246 Thr Val Ala Val Arg Ser Pro Ser Met Asn Val Ala Leu Tyr Val Gly
247 225             230             235             240
248 Ile Ala Val Gly Val Val Ala Ala Leu Ile Ile Ile Gly Ile Ile Ile
249             245             250             255
250 Tyr Cys Cys Cys Cys Arg Gly Lys Asp Asp Asn Thr Glu Asp Lys Glu
251         260             265             270
252 Asp Ala Arg Pro Asn Arg Glu Ala Tyr Glu Glu Pro Pro Glu Gln Leu
253         275             280             285
254 Arg Glu Leu Ser Arg Glu Arg Glu Glu Glu Asp Asp Tyr Arg Gln Glu
255     290             295             300
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268 ggggatctta ctgggcctgc tactcctggg gcacctaaca gtggacactt atggccgtcc 180
269 catcctggaa gtgccagaga gtgtaacagg accttggaaa ggggatgtga atcttccctg 240
270 cacctatgac cccctgcaag gctacaccca agtcttggtg aagtggctgg tacaacgtgg 300
271 ctcagaccct gtcaccatct ttctacgtga ctcttctgga gaccatatcc agcaggcaaa 360
272 gtaccagggc cgcctgcatg tgagccacaa ggttccagga gatgtatccc tccaattgag 420
273 caccctggag atggatgacc ggagccacta cacgtgtgaa gtcacctggc agactcctga 480
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VERIFICATION SUMMARY   DATE: 04/06/2005
PATENT APPLICATION: US/10/785,220A   TIME: 14:13:58

Input Set : **A:\39780-1216.TXT**
Output Set: **N:\CRF4\04062005\J785220A.raw**